

OM protein - protein search, using sw model

Run on: August 3, 2005, 15:09:22 ; Search time 124.164 Seconds  
(without alignments)  
1102.679 Million cell updates/sec

Title: US-10-670-863-1  
Perfect score: 1927  
Sequence: 1 MTAKPLRRTLVSLLFFALSGV.....KNHYIQAFHKLYLRYGFCK 354

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\* )  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

OM protein - protein search, using sw model

Run on: August 3, 2005, 15:22:29 ; Search time 27.4746 Seconds  
(without alignments)  
1239.716 Million cell updates/sec

Title: US-10-670-863-1  
Perfect score: 1927  
Sequence: 1 MTAKPLRRTLVSLLFFALSGV.....KNHYIQAFHKLYLRYGFCK 354

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

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OM protein - protein search, using sw model

Run on: August 3, 2005, 15:10:36 ; Search time 123.636 Seconds  
(without alignments)  
1466.210 Million cell updates/sec

Title: US-10-670-863-1  
Perfect score: 1927  
Sequence: 1 MTAKPLRTVLSLLFFALSGV.....KNHYIQAFHKLYLRYGFCCK 354

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

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OM protein - protein search, using sw model

Run on: August 3, 2005, 15:09:22 ; Search time 110.836 Seconds  
(without alignments)  
1102.679 Million cell updates/sec

Title: US-10-670-863-1\_COPY\_1\_316  
Perfect score: 1712  
Sequence: 1 MTAKPLRTVLSLLFFALSGV.....DHSKWCVSIKGSANRWTCIG 316

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

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OM protein - protein search, using sw model

Run on: August 3, 2005, 15:22:29 ; Search time 24.5254 Seconds  
(without alignments)  
1239.716 Million cell updates/sec

Title: US-10-670-863-1\_COPY\_1\_316  
Perfect score: 1712  
Sequence: 1 MTAKPLRRTVLSLLFFALSGV.....DHSKWCVSIKGSANRWTCIG 316

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

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OM protein - protein search, using sw model

Run on: August 3, 2005, 15:10:36 ; Search time 110.364 Seconds  
(without alignments)  
1466.210 Million cell updates/sec

Title: US-10-670-863-1\_COPY\_1\_316  
Perfect score: 1712  
Sequence: 1 MTAKPLRRTVLSLLFFALSGV.....DHSKWCVSIKGSANRWTCIG 316

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

OM protein - protein search, using sw model

Run on: August 3, 2005, 14:59:46 ; Search time 32.2299 Seconds  
(without alignments)  
819.916 Million cell updates/sec

Title: US-10-670-863-1  
Perfect score: 1927  
Sequence: 1 MTAKPLRTVLSLLFFALSGV.....KNHYIQAFHKLYLRYGFCK 354

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

OM protein - protein search, using sw model

Run on: August 3, 2005, 15:08:42 ; Search time 113.597 Seconds  
(without alignments)  
1214.127 Million cell updates/sec

Title: US-10-670-863-1  
Perfect score: 1927  
Sequence: 1 MTAKPLRTVLSLLFFALSGV.....KNHYIQAFHKLYLRYGFCK 354

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*  
 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*  
 17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep:\*  
 18: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
 19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep:\*  
 20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

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OM protein - protein search, using sw model

Run on: August 3, 2005, 15:02:41 ; Search time 373.021 Seconds  
 (without alignments)  
 1108.448 Million cell updates/sec

Title: US-10-670-863-1  
 Perfect score: 1927  
 Sequence: 1 MTAKPLRTVLSLLFFALSGV.....KNHYIYQAFHKLYLRYGFCK 354

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:\*  
 1: /cgn2\_6/ptodata/1/paa/PCTUS\_COMB.pep:\*  
 2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/1/paa/US080\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/1/paa/US081\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/1/paa/US082\_COMB.pep:\*  
 7: /cgn2\_6/ptodata/1/paa/US083\_COMB.pep:\*  
 8: /cgn2\_6/ptodata/1/paa/US084\_COMB.pep:\*  
 9: /cgn2\_6/ptodata/1/paa/US085\_COMB.pep:\*  
 10: /cgn2\_6/ptodata/1/paa/US086\_COMB.pep:\*  
 11: /cgn2\_6/ptodata/1/paa/US087\_COMB.pep:\*  
 12: /cgn2\_6/ptodata/1/paa/US088\_COMB.pep:\*  
 13: /cgn2\_6/ptodata/1/paa/US089\_COMB.pep:\*  
 14: /cgn2\_6/ptodata/1/paa/US090\_COMB.pep:\*  
 15: /cgn2\_6/ptodata/1/paa/US091\_COMB.pep:\*

16: /cgn2\_6/ptodata/1/paa/US092\_COMB.pep:\*  
 17: /cgn2\_6/ptodata/1/paa/US093\_COMB.pep:\*  
 18: /cgn2\_6/ptodata/1/paa/US094\_COMB.pep:\*  
 19: /cgn2\_6/ptodata/1/paa/US095\_COMB.pep:\*  
 20: /cgn2\_6/ptodata/1/paa/US096\_COMB.pep:\*  
 21: /cgn2\_6/ptodata/1/paa/US097A\_COMB.pep:\*  
 22: /cgn2\_6/ptodata/1/paa/US097B\_COMB.pep:\*  
 23: /cgn2\_6/ptodata/1/paa/US098\_COMB.pep:\*  
 24: /cgn2\_6/ptodata/1/paa/US099A\_COMB.pep:\*  
 25: /cgn2\_6/ptodata/1/paa/US099B\_COMB.pep:\*  
 26: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep:\*  
 27: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep:\*  
 28: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep:\*  
 29: /cgn2\_6/ptodata/1/paa/US103\_COMB.pep:\*  
 30: /cgn2\_6/ptodata/1/paa/US104\_COMB.pep:\*  
 31: /cgn2\_6/ptodata/1/paa/US105\_COMB.pep:\*  
 32: /cgn2\_6/ptodata/1/paa/US106\_COMB.pep:\*  
 33: /cgn2\_6/ptodata/1/paa/US107\_COMB.pep:\*  
 34: /cgn2\_6/ptodata/1/paa/US108\_COMB.pep:\*  
 35: /cgn2\_6/ptodata/1/paa/US109\_COMB.pep:\*  
 36: /cgn2\_6/ptodata/1/paa/US110\_COMB.pep:\*  
 37: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep:\*

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OM protein - protein search, using sw model

Run on: August 3, 2005, 15:05:27 ; Search time 47.5522 Seconds  
 (without alignments)  
 1072.555 Million cell updates/sec

Title: US-10-670-863-1  
 Perfect score: 1927  
 Sequence: 1 MTAKPLRTVLSLLFFALSGV.....KNHYIYQAFHKLYLRYGFCK 354

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 664618 seqs, 144074520 residues

Total number of hits satisfying chosen parameters: 664618

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Pending\_Patents\_AA\_New:\*  
 1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep:\*  
 2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep:\*  
 7: /cgn2\_6/ptodata/2/paa/US11\_NEW\_COMB.pep:\*  
 8: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep:\*

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OM protein - protein search, using sw model

Run on: August 3, 2005, 14:59:46 ; Search time 28.7701 Seconds  
(without alignments)  
819.916 Million cell updates/sec

Title: US-10-670-863-1\_COPY\_1\_316  
Perfect score: 1712  
Sequence: 1 MTAKPLRTVLSLLFFALSGV.....DHSKWCVSIKGSANRWTCIG 316

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

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OM protein - protein search, using sw model

Run on: August 3, 2005, 15:08:42 ; Search time 101.403 Seconds  
(without alignments)  
1214.127 Million cell updates/sec

Title: US-10-670-863-1\_COPY\_1\_316  
Perfect score: 1712  
Sequence: 1 MTAKPLRTVLSLLFFALSGV.....DHSKWCVSIKGSANRWTCIG 316

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep: \*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep: \*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep: \*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep: \*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep: \*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep: \*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep: \*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep: \*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep: \*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep: \*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep: \*  
17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep: \*  
18: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep: \*  
19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep: \*  
20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep: \*  
21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep: \*  
22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep: \*

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OM protein - protein search, using sw model

Run on: August 3, 2005, 15:02:41 ; Search time 332.979 Seconds  
(without alignments)  
1108.448 Million cell updates/sec

Title: US-10-670-863-1\_COPY\_1\_316  
Perfect score: 1712  
Sequence: 1 MTAKPLRTVLSLLFFALSGV.....DHSKWCVSIKGSANRWTCIG 316

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:\*

1: /cgn2\_6/ptodata/1/paa/PCTUS\_COMB.pep: \*  
2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/paa/US080\_COMB.pep: \*  
5: /cgn2\_6/ptodata/1/paa/US081\_COMB.pep: \*  
6: /cgn2\_6/ptodata/1/paa/US082\_COMB.pep: \*  
7: /cgn2\_6/ptodata/1/paa/US083\_COMB.pep: \*  
8: /cgn2\_6/ptodata/1/paa/US084\_COMB.pep: \*  
9: /cgn2\_6/ptodata/1/paa/US085\_COMB.pep: \*  
10: /cgn2\_6/ptodata/1/paa/US086\_COMB.pep: \*  
11: /cgn2\_6/ptodata/1/paa/US087\_COMB.pep: \*  
12: /cgn2\_6/ptodata/1/paa/US088\_COMB.pep: \*  
13: /cgn2\_6/ptodata/1/paa/US089\_COMB.pep: \*  
14: /cgn2\_6/ptodata/1/paa/US090\_COMB.pep: \*  
15: /cgn2\_6/ptodata/1/paa/US091\_COMB.pep: \*  
16: /cgn2\_6/ptodata/1/paa/US092\_COMB.pep: \*  
17: /cgn2\_6/ptodata/1/paa/US093\_COMB.pep: \*  
18: /cgn2\_6/ptodata/1/paa/US094\_COMB.pep: \*  
19: /cgn2\_6/ptodata/1/paa/US095\_COMB.pep: \*



20: /cgn2\_6/ptodata/1/paa/US096\_COMB.pep:\*  
 21: /cgn2\_6/ptodata/1/paa/US097A\_COMB.pep:\*  
 22: /cgn2\_6/ptodata/1/paa/US097B\_COMB.pep:\*  
 23: /cgn2\_6/ptodata/1/paa/US098\_COMB.pep:\*  
 24: /cgn2\_6/ptodata/1/paa/US099A\_COMB.pep:\*  
 25: /cgn2\_6/ptodata/1/paa/US099B\_COMB.pep:\*  
 26: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep:\*  
 27: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep:\*  
 28: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep:\*  
 29: /cgn2\_6/ptodata/1/paa/US103\_COMB.pep:\*  
 30: /cgn2\_6/ptodata/1/paa/US104\_COMB.pep:\*  
 31: /cgn2\_6/ptodata/1/paa/US105\_COMB.pep:\*  
 32: /cgn2\_6/ptodata/1/paa/US106\_COMB.pep:\*  
 33: /cgn2\_6/ptodata/1/paa/US107\_COMB.pep:\*  
 34: /cgn2\_6/ptodata/1/paa/US108\_COMB.pep:\*  
 35: /cgn2\_6/ptodata/1/paa/US109\_COMB.pep:\*  
 36: /cgn2\_6/ptodata/1/paa/US110\_COMB.pep:\*  
 37: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep:\*

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OM protein - protein search, using sw model

Run on: August 3, 2005, 15:05:27 ; Search time 42.4478 Seconds  
 (without alignments)  
 1072.555 Million cell updates/sec

Title: US-10-670-863-1\_COPY\_1\_316  
 Perfect score: 1712  
 Sequence: 1 MTAKPLRTVLSLLFFALSGV.....DHSKWCVSIKGSANRWTCIG 316

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 664618 seqs, 144074520 residues

Total number of hits satisfying chosen parameters: 664618

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Pending\_Patents\_AA New:\*  
 1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep:\*  
 2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep:\*  
 7: /cgn2\_6/ptodata/2/paa/US11\_NEW\_COMB.pep:\*  
 8: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep:\*

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 22:22:19 ; Search time 294.332 Seconds  
 (without alignments)